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	Saci 95 105 115 125 135 145 85 85 GAGGCTCGAGGCTCCACGAGTTAGACTCCACTCAGAGGCTGACTCCAGGG
	XhoI 170 180 190 200 210 220 160 160 160 160 170 160 180 180 200 210 220
	GTCTACACCTCTAAGGGCGACACTGGGCLLCAAGCACACTGGGGTGGGG
	CACCAGCCCGCAGAGCTAGGTTGGGTGGACALTAGGGTGGTTGGTGGTGGAGGTGGGGGGGGGG
	CCAGCICCIICICCCCCCCCCCCCCCCCCCCCCCCCCCC
	GGGAACTITITCCAGAAGICICIAIGACTITITAGITITGGGTCACTITGCCCTICCTGAACCACTICCTGAC 630 610 610 620 630 650 650 650
	Apall EspI 715 725 735 745 745 725 735 745 TGACATTGCAGGCATTGCAGGCAAACGCAC TGACATTGCAGGCAGGCAAACGCAC
	760 770 780 800 820 820 Argcaagagcccrgcccrgcccrgcccrgcccrgcccrgc

CTAGGAAAAAAGCAATCCCTCTGTTGTGGGAGGAAGGTTGCAGTGTGTGT	STCTGTTGTG 995 STTTACAAGT	000	C C C	GGCACACACCTIGGGCCTGCTCTGAGTATGACAGAGCCCCTTGGGAAGTTGTAGGTGGAGGAGGAAGAAAAATGA	050	0.70	
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1060 10 CTGTATCATTTTCAC 1135 11		GCTCAGGCCC	CTGACCCGAATG BSmI+	GCTTCCAAA1	TTACGTAGT	TCTGGAAA	
CTGTATCATTITCAC 1135 TGTCTCATTICTICT	1070	1080	1090	1100	1110	1120	
TGTCTCATTTCTTCT	TACTCAAA 45	GAAACCTCGC 1155	GGAGTGTTTTC 1165	TTCTGAAAGG 1175	TCATCAGGT 1185	TTTGACTC 1195	
	rccrecre	GTGGTGATG(3TTGCTTGTCC	CAGGCCCTGT	CCCCCATCC	rcrrgccc	Serial Atty I Atty/
1210 12	1220	1230	1240	1250	1260	1270	tor(: No Doc! Age:
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rgtgag	TGGAGGGG	TTTCGATTC	CTTATGGAAT	CCAGGCAGAT	GTAGCATTTA	AAACAACA	man t Ass STK- ck R.
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1435 14	1445	1455	1465	1475	1485	1495	ler)64
TGGGGCATTGGCACCTCCC TTAGTAGGGCCTTTGCTGGGGGTAGAATGAGTTTTAAGGCAGGTTAGAGCTTTAGACCCTCGA BSpMl-	TAGTAGGG	CTTTGCTG	SGGGTAGAAAT	GAGTTTTAAG	SCAGGTTAG BSPMI-	ACCCTCGA	5US
1510 15	1520	1530	1540	1550	1560	1570	
ATCGGG	ATTTACCC	CCCAGCCGT	rcrgrgcrrca	TTGCTGTTCA	CATCACTGC	CTAAGATG	•
1585 15	1595	1605	1615	1625	1635	1645	
rgrgrg	TGTTTCTT	TCTCCTCAC	regerrerect	TCTTCACTTC	CTTGTCAAT	GCAGAGAA	i
1660 1670	70	1680	1690	1700	1710	1720	
CAGCAGCAGCACCAGAGG CCTGTAAGAAGCACGAGGTGTATGTCAGCTTCCGAGACCTGGGCTGGGCAGA Stut	AGGCCTTG Stut	TAAGAAGCAG	GAGCTGTATG	TCAGCTTCCC	AGACCTGGG	CTGGCAGG BSPMI	
1735 1745 1755 1765 1775 1785 1795	1745	1755	1765	1775	1785	1795	

ApaI EcoO

GCCTCGCTAGGAAGGGTACTTGGCTAAGGA 1925 1935 1945GGGAGCCAGCATGGTGATGCCATTATGA 2000 2010 2020 TTGTTTAAGGTGAACTGCCAGTGTGACCA 2075 2085 2095 CCTGTGCCGCGTTCTGTCCAGACACAGC	N 2160 2170 TATGTTTTTAGAAATGGG	2235 2245 FTTGACGCCGTCTTCCCACT	Tthilli 2310 2320 CTITTGGGACCATGAGAGG	2385 2395 CTTTCACCTTGGTCGTGAG	2460 2470 TGGTTTCCCACACTCTTT 2535 2545 GGGGAGTGCCTTCCCTC	2610 2620 ACGCCATCTTGGGGTGTGG	2685 2695 CTGAGTAGATGTCAGCCC
1820 1830 1870 1870 1870 1850 1870 1895 1895 1905 1905 1905 1915 1925 1935 1945 1945 1970 1970 1980 1980 2000 2000 2010 2020 2010 2020 2010 2020 2010 2020 2010 2020 2010 2020 2010 2020 2010 2020 2010 2020 2010 2020 2045 2045 2055 2065 2075 2085 2095 Pf1 Saci	2120 2130 2140 2150 2160 2160 2160 2170 ETTAGGATCAGCCCCCCCTCTTCATTTTTATTTTTTTTAGAAATGGG	2195 2205 2215 2225 2235 2245 CCCAGGCTGGGTGCTGTGATCATAGCTCACCGCAGCTTTGACGCCGTCTTCCCACT	2280 2290 2300 AGACTATAGAGTGGTCCTTCTTTCCAT	2355 2365 2375 CCTGCTGCTCAGAAGGCATGGTCTGAGG	GGATGC	2570 2580 2590 2600 2610 2620 ACGCCACCAACCACCATCGTGCAGCCTGGTGGTGTCACGCCATCTTGGGGTGTGA	is 2665 2675 AGATCCTGCTGCTCCAAGCTGGGGC
GTCTTGTTTCTCATCTCTCCCAGTTAAGAGTCCAGTATCAAGTGGCTTGGCTAGGGAAGGGTACTTGGCTAAGGA 1885 1895 1905 1915 1925 1925 1945 1960 1970 1970 1980 1980 1990 2000 2010 2020 2020 2020 2020 202	2110 rGGATGTCCAT	ฮ์	GG	CCACCCATGITICCTGCCCTGCTGGGCCCTGCTCAGAAGGCATGGTCTGAGGCTTTCACCTTGGTCGTGGGCCTTGGTCGTGGTCTGAGGCTTTCACCTTGGTCGTGAG	_ F. F.	2560 2570 2580 TGAACTCCTACATGAACGCCACCAACCACGCC	2635 2645 2665 2665 2675 2685 2695 TCACCTGGGCCGGGCCACCACCAGATCCTGCTGCCTCCAAGCTGGGGCCTGAGTAGATGTCAGCCC tEII Bg11 Ecol
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2770 CTGG	28 AAG	2920 rgcr	2995 CCAG 3070 GGAA	3145 3220 TTAT	3295 TAGT	3370 GTCC 3445 TTTG 3520 GCCT(3595 TGTG
TGA	TÅA	ည်)		, <u>1</u>	CTG
TTA	5 AAC	255	Apai Ecoo 5 AAGC 0 GTCA(BstEII 35 GCTCTG 10 GACCTT	<u>5</u>	TCC GGG CAA
2760 TACT	2835 AGTA	2910 ACTG	A) 2985 CAGA 3060 CGGG	BSt 3135 CTGCT 3210 AGGAC	ECOO 3285 TGAAT BSMI	3350 3435 GGCAG 3510 AACTT 3585 CTGGA
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S S S	2825 TAAT	2900 GCCIA	2975 GCACA 3050 AAATT	3125 GGTGT 3200 CCAAG	75	25 25 25 75 75 75 75
AAT		25 3TGC	29 3660 30	31 32 32 TCC	3275 CCACC	3425 3425 16CTC 3500 1CCTC 3575
AAA	TTC	A CG(SAGC	AGT.	CAT	CTG TTC CCC
TAAAA	2815 TTAT	2890 rggrr	Apal EcoO CAGATGAGAAATTTCAGTGAGGGGCACAGTGATCAGAAGCGGGCCAGGGGGACAGGGGCCACAGTGAGGGGCACAGTGATCAGAAGCGGGCCAGGGGGGGG	LS ACTO	SS GAT	AAT 5 TGA 0 CTC
iri	2 PATT	28 CTG	2965 TTCAG 3040 CATTT	3115 3ACAC 3190 FTGCT	3265 FACTG	3340 3415 3415 3490 3490 316C 17CCC
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SCC	3ACC	GTA	CAG	SCCCAGICA 3105 3180 3GATTITGE	်ည	SCTC
GGGGC	EC00 95 TTCG	GTA	AAA TGG	GTG AGG	TGA(CTC CTC GGT
ATTGCCATGTCATGACTTTTGGGGGCCCCTTGCGCCGTTAAAAAAAA	ECOO 2785 2795 2805 2815 2825 2835 2845 GGTATAAAGAGGAGTATTTCTCCTAATTTTTAAAGTAACTAAAGTTGT	2860 2870 2890 2890 2900 2910 2920 ATGGGCTCCTTTGAGGATGCTTGTAGTATTGTGGGTGCTGGTTACGGTGCCTAAGAGCACTGGGCCCCTGCTTCA	Apal EcoO 2935 2945 2955 2965 2975 2985 2995 TTTTCCAGTAGGAAACAGGTGAGAAATTTCAGTGAGGGGCACAGTGAAACAGGGGCCACAGGGGCACAGGGGCCACAGGGGCACAGGGGCCACAGGGGGCACAGGGGGCACAGGGGGCCACAGGGGGCACCCAGGAGCGGGCCAGGAGG	3085 3095 3105 3115 3125 3135 3145 TCCATGTGATAATGAGATTAACGTGCCCAGTCACGCGACACTCTCAGTATTCCTGCTCTGCCCAACAGCA 3160 3170 3180 3190 3200 3210 ACCATAGTTGATAAGAGCTGTTAGGATTTTGTCCTTTTGCTTAGAATCCAAGGGTCAAGGTTCAAGGACCTTGGTTATGTTA	3245 CATC 3320	ACCAGGACTACTCCCTCTTTTAGTAATCTGCCTCCTTTTTCTTGTCCCTGTCCTGT 3395 3405 3415 3425 3435 3445 GGAGAAAAATCTCATTTTCATTTGATTCTGCTCTTTTTTTT
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<u> </u>	2785 GAGGA	2860 CTTT	2935 TAGA 3010 GATG	3085 ATAA: 3160 TGAT	3235 TCAT 3310	CACTACCAGG 3385 STCCTGGAGAA 3460 GTTTTTTTAA 3535 AAGGTCCTTA ECOOMSTII
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1 GC	ľAĽ	3666	TCC	'ATG 'ATA	Ü	GAGC Saci TTAA TGTT: GATT(
AT	99	AT	GAT	700 A00	3235 3265 3265 3275 EcoO GCTCCCTGTCATGAACATCTGAGCCTTTCCTGCCTACTGATCATCCTGCCTTGACTCTACTAGTGAC 3310 3320 3330 3330	AGAGACTCACTACCAGGACTACTCCTTTTCATTTAGTAATCTGCCTCCTTTTCTTTGTCCTGTCCTGT Saci 3385 3395 3405 3415 3425 3435 3445 GTGTTAAGTCCTGGAAAAATCTCATCTATCCTTTTGATTCTGCCTCTTTTGTTTTTTTT

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AACCC 45 GAGAT B91I 3820 ACTGT	SAAG SAAG	CAG	TTT GTG CTG	AAA CAC Bs
3670 TCCAA 3745 CCAGA B 383	3895 2ATTC 3970 AGCAT	Sphi 4045 CCTA(4120 ACGT(4195	4270 GGCA 4345 TCTA 4420 GGTC	4495 CTGC 4570 GTGT(
CTTC TTCA	AAAT(AAAA	GAAC	CATA	FTGT,
3660 3735 3735 AGTATT 3810 TAAAAG	3885 CTTTA DraI 3960 TGTGT	4035 AAGCC1 4110 TGTCTT 4185	4260 GGCACT 4335 ATGGAG 4410 AGAATT	4485 TTCCCC 4560 GGCTTG
36 ATCTCJ 37 SATCAG CGTTTA	TTGC	CTCA 43 CCCTC	42 26 43 24 24 24 24	44 TGTT 45
550 350 255 CTTCC 3800 GTCAT	75 3GAAT 10 CATA	5 GATG 0 CTGG 5 5	CTCA(s rectt ogrec
3650 3650 3725 3725 CCTACT 38(3875 3GCTGG/ 3950 FCCATC/	4025 CCACTGI 4100 ATCTCT 4175 GTGGCC	4250 GGACC 4325 CCATG 4400 TTCCC	4475 TCTAT(4550 AGGGA(
140 CTGCCA 15 TGTGCA APali APali 3790 TGCGAT	TGAT(ATTG:	CCAGI STGGA	rcagt Baagt GCAG	AACC
3620 3630 3640 3650 3660 3670 TGGAAGGTGCCAGGCTTCCCCGGCTGCCAGGGACACCTTCTTCCTTC	3845 3855 3865 3875 3885 3895 TGATGAAATGCTTCCAGAGGAAATGACTGGCTGGAATTTGCTTTAAAATCATTCAAG Drai 3920 3930 3940 3950 3960 3970 GAAGGGTATGGATGTGTAAAAGCATGCT	3995 4005 4015 4025 4035 4045 GTCACAGCCTGGAGCTGATGCTCAAGCCTAGGCACCTACAG 4045 4070 4080 4100 4110 4120 4120 4120 4120 4120 4120 4125 4155 4165 4195 4195 6195 667TCGTTTGGTTTGGTTTGCTTTGTTTGTTTGTTTGTTTAGT	4240 4315 4315 CAGAC 4390 ACAGG	A445 A455 4465 4475 4485 4495 CCCTTCCTTCCCACTGTATATGTGAAAACCTCTATGCTTTGTTCCCTTGTAAAAAAAA
TCCC	gaaa) 3agtt	AACAG AACAG	TTTG	APALI 4 TAATG AAGTG
3630 ATGTCT 3705 3705 3780 3780	3855 CAGAG 3930 TGTAA	4005 GTGGTV 4080 AAAACZ 4155 TGCCGT	4230 GTCTAT 4305 CTGTAA 4380 TCTACA	4455 ACTGTA 4530 CATGTA
AGGCZ SAGTC	3 PTTCC	GAGG 4 TTGA 4 GGCT	45 TCGGJ CCTCJ 43 CAATC	44 2CCAC 45 3TCCA
520 51GCC 595 AACAG 3770 CTCC	45 AATGC 20 FATGC	95 SCCTG 70 CACG 15	O TACC S ACAT O TCAG	S CTTC(0 AGTTC
36 36 36 37 36 30 30 30 30 30 30 30 30 30 30 30 30 30	3845 ATGAAA: 3920 AGGGTAJ	3995 CACAGC 4070 AGTITC 4145 ATCTTGC	4220 4295 3TCCCA(4370 CTATT	4445 CTTCC 4520 ACTGA(
S10 SCCTGGA 185 GGCCCAT NCOI 3760 AAAGTGA	i rccre	CAGT	CTATT	3GCCC 3CAGA
358 368 368 CATG	3835 AGAGAGT I 3910 GCAGGTGG	3985 37CAGC 4060 AAACCC 4135 TAACA	4210 4285 4285 IGTGTC 4360 3TCAGC	4435 ATCTC 4510 AATCC
1A-5 ₃₆₁₀ TGCCAGTATCCCC 3685 CTGCCTTCATGGC Bgll 3760 CTGCAGGATCAAG		GGCCTATGTCAGCAGTCACAGCCTGGAGTGGTAACAGAGTGCCAGTCACTGATGCTCAAGCCTGGCACCTACAG 4060 4070 4080 4090 4100 4110 4110 4120 TTGCTGGAAACCAGAAACTTTCACGTTGAAAACAACAGGACAGTGGAATCTCTGGCCCTGTCTTGAACACGTGGCACGTGGCAAGCCTGCTTGAACACGTGGACAGTGGAATCTCTGGCCCTGTCTTGAACACGTGGCACAGTGGAATCTCTGGCCTTTGAACACGTGGCACAGTGGAATCTCCTTGAACACACGTGGCAGAAACAAAACAACAGAAAACAAAAAAAA	E E E	4435 AATGTCGGATCTGGC 4510 ACAGGGATAATCCCA
TA: TGCC TGC TGC Bg CTGC I	CTT X GTG	GGCCI TTGCT AGATC Bqlii	CCCC	AATG
FIG. 1A-5 3610 3620 3630 3640 3650 3660 3670 TGCCAGTATCCCTGGAAGGTGCCAGGCATGTCTCCCCGGCTGCCAGGGGACACTCTTCTTCCAACCC 3685 3705 3715 3725 3735 3745 CTGCCTTCATGGCCCATGGAACAGGAGTGCCATCGCCTGTGTGCACCTTCCATCTTCACTATCTTCACAGAGTT Apali Apali Bg11 Bg11 3760 3770 3780 3790 3800 3810 3820 CTGCAGGATCAAAGTGAATTGTGAAATGATGCGATTGTGGATTGTGGTCATGTTTAAAAGGGGGCAACTGT Bst. I ECORI				
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FIG. 1A-6

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4645	ACTCACCGCT	
4635	AGTTAGAACC	
4625	ACGTGGAGGCCAGT	
4615	CATAGA	
4605	AGGATGTTTCTT	
4595	TATGCCCAGACA	
4585	TGCAGTCATTCATTA	MI+

 4660
 4670
 4680
 4690
 4710
 4720

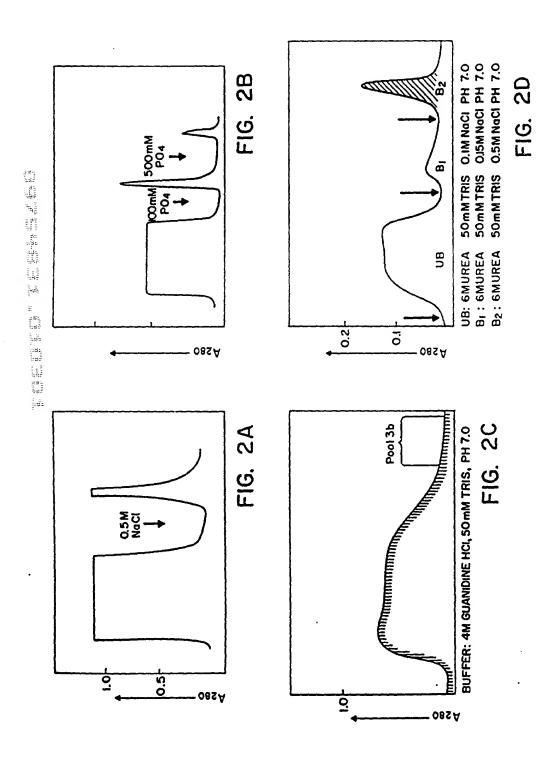
 TCTCACCACTGCCCACGGAAACGGTGCCCAAGCCCTGCT

 CTGC PMI+ Psti

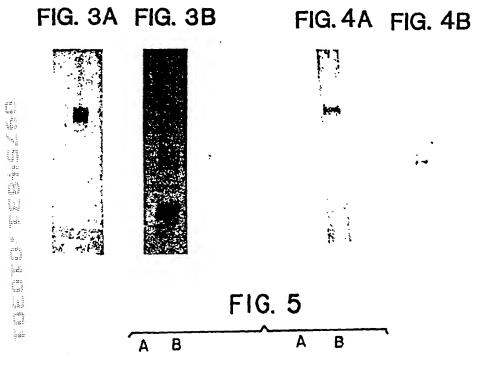
GAAACATGGTGCTGGGCCTGTGGCTGCCACTAGCTCCTCCGA

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CONSENSUS PROBE 20 30 40 50 60 70 GATCCTAATGGGCTGTACGTGGACTTCCAGCGCGACGTGGGACGACTGGATCATCGCCCCCGTCG ** TGTAAGAAGCACGAGCTTCCGAGACCTGGGCTGGCACGACTGGATCATCGCCCCCGTCG ** TGTAAGAAGCACGAGCTGTATGTCAGCTTCCGAGACCTGGGCTGGCAGGACTGGATCATCGCGCCTGAAG OP4 28 58 88	ACTTCGACGCCTACTACTGCTCCGGAGCCTGCCAGTTCCCCTCTGCGGATCACTTCAACAGCAACCA ** **	150 160 170 180 190 200 210 CGCCGTGGTGCAGCCCTGGTGAACAACATGAACCCCGGCAAGGTACCCAAGCCCTGCTGCTGCCCACC **** ******* ***** **************	GAGCTGTCCGCCATCAGCATGCTGTACCTGGACGAGAATTCCACCGTGGTGCTGAAGAACTACCAGGAGA **** ***** **** ** ** ** ** *** CAGCTCAATGCCATCCTCTACTTCGATGACTCCTCAACGAACTACCAGGAGA **** ***** **** *** *** *** *** *** *	290 310 TGACCGTGGGCTGCCGCTAACTGCA ** ** ** ** ** ** ** TGGTGGTCCGGGCCTGCCACTAGCTCCT 308 318 328
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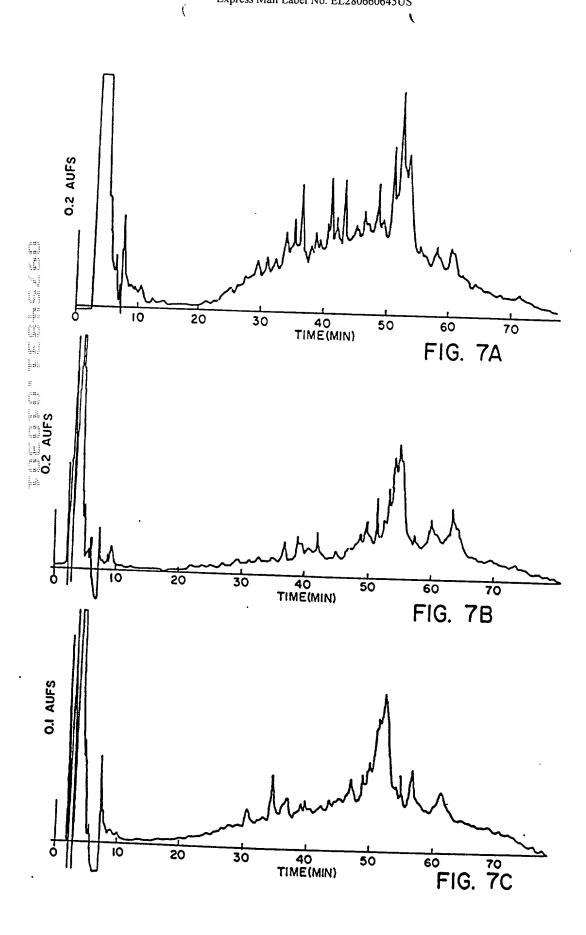


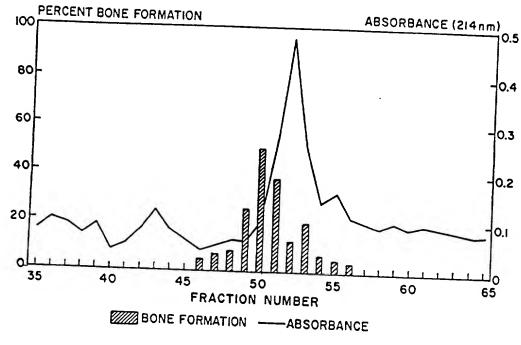
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FIG.6 A FIG.6 B FIG.6 C FIG.6 D FIG.6 E

FIG. 15

- NON-REDUCIBLE 30K
- 18K SUBUNIT
- 16K SUBUNIT





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FIG. 8

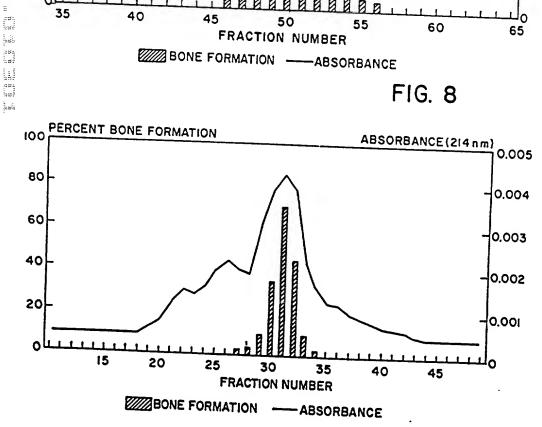
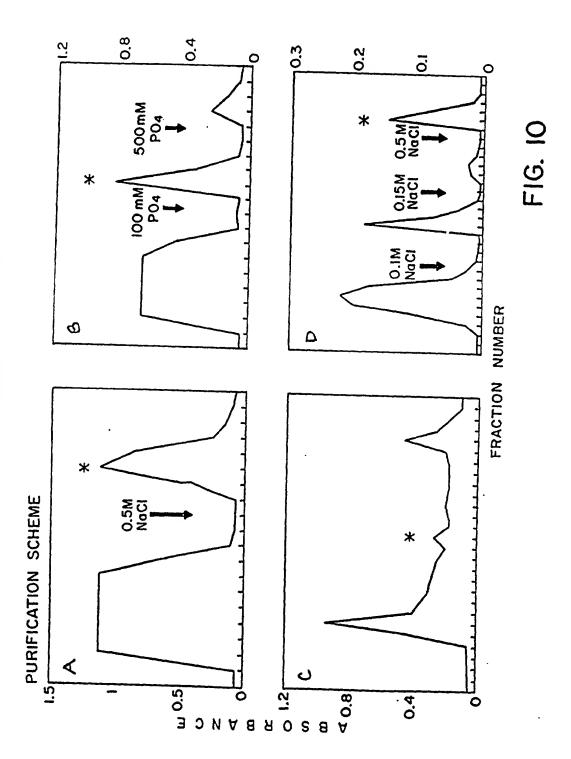


FIG. 9

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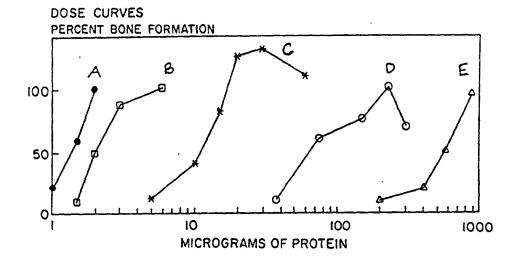


FIG. 11

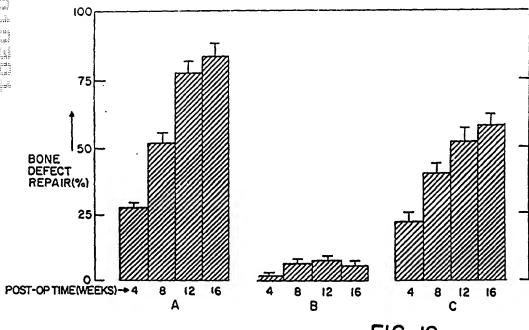


FIG. 12

FIG. 13

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E)	P	•	N		G		L	3	•	V		D		F	(2	R	•	D		V	(;	H	7	D	D)
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CG	T	C	C	:A	CC	G/	\G	CT	GI	C	CG	CC	A	C	AG	CZ	T	GC	TC	T	AC	CT	G(3A	CG	A	A	ATT	ŧ
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CC	A	CC	G7	CG	GI	G(T	GA	AG	W	4C	TA	C	CA	GG	A	3A'	TG	AC	:C	GT	GG	T	G	GC	T	C	GGC	
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310 TGCCGCTAACTGCAG C R *

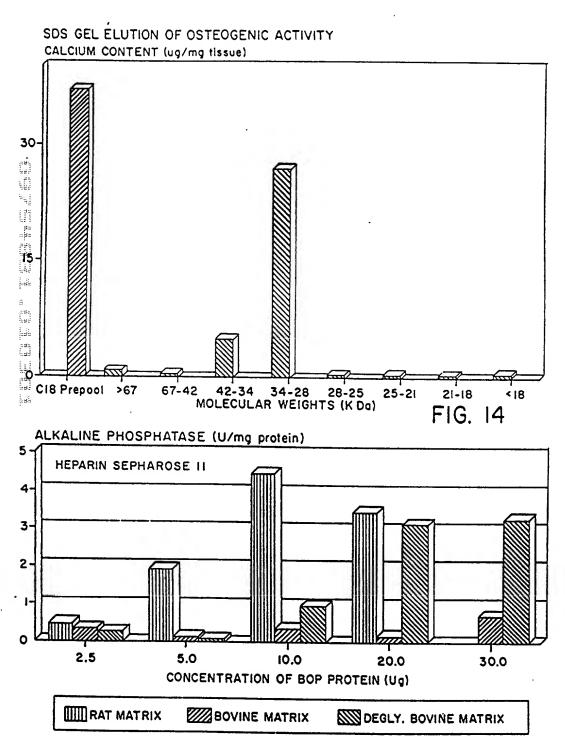
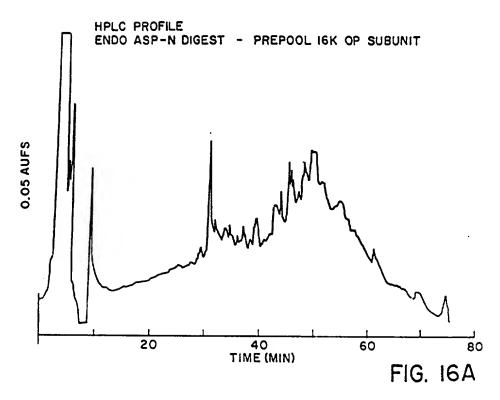
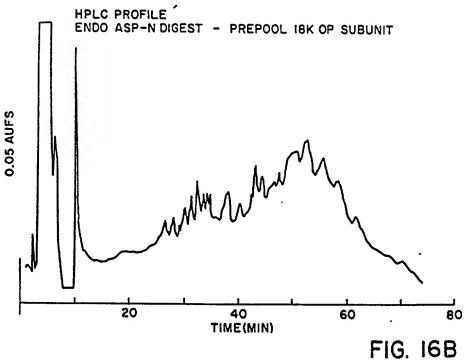


FIG. 19

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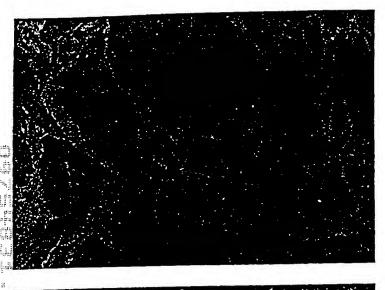


FIG. 17A

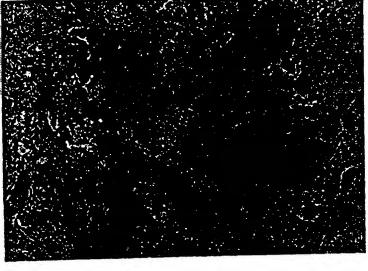


FIG. 17B

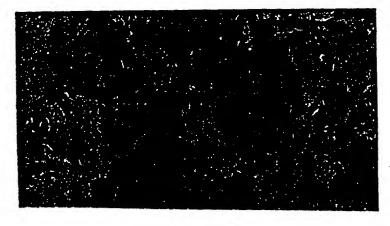


FIG. 17C

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FIG. 18-2

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FIG. 18-4

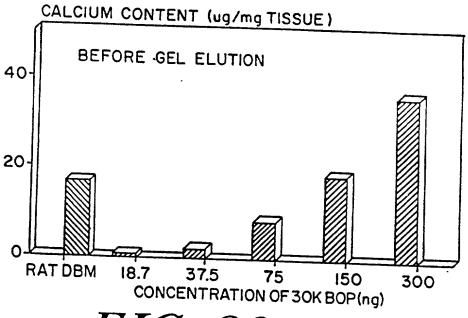


FIG. 20A

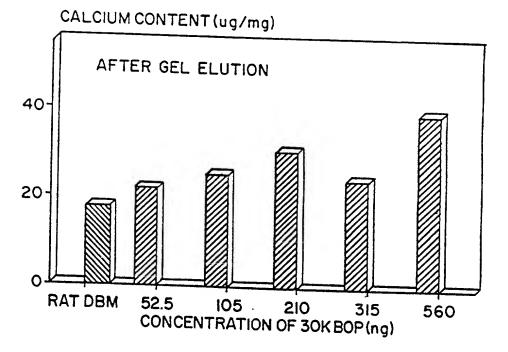


FIG. 20B

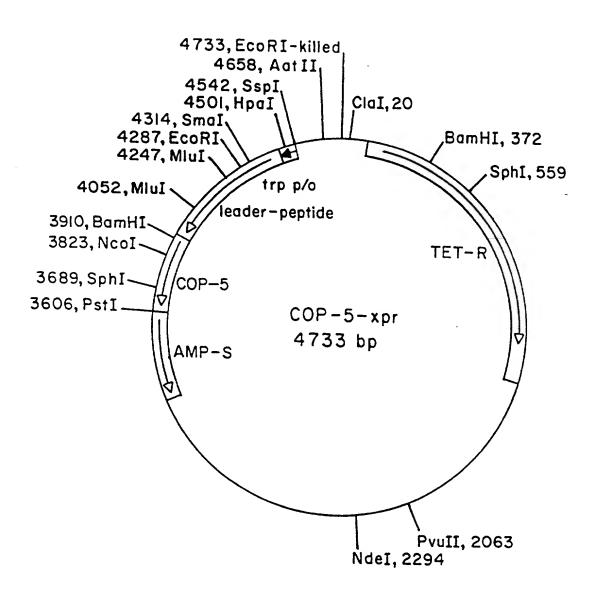


FIG. 21A

Inventor(s):Oppermann et al.
Serial No. Not Yet Assigned
Atty Docket No. STK-008CN

COP-5 fusion protein

Atty/Agent: Patrick R. H. Waller
Express Mail Label No. EL280660645US

10 20 30 40 50
ATGAAAGCAATTTTCGTACTGAAAGGTTCACTGGACAGAGATCTGGACTC
M K A I F V L K G S L D R D L D S
Bglii

60 70 80 90 100
TCGTCTGGATCTGGACGTTCGTACCGACCACAAAGACCTGTCTGATCACC
R L D L D V R T D H K D L S D H

110 120 130 140 150
TGGTTCTGGTCGACCTGGCTCGTAACGACCTGGCTCGTATCGTTACTCCC
L V L V D L A R N D L A R I V T P
Sall Sma

160 170 180 190 200
GGGTCTCGTTACGTTGCGGATCTGGAATTCAA
G S R Y V A D L E F M A D N K F N
I ECORI

210 220 230 240 250
CAAGGAACAGCAGAACGCGTTCTACGAGATCTTGCACCTGCCGAACCTGA
K E Q Q N A F Y E I L H L P N L
MluI BglII BspMI+

260 270 280 290 300
ACGAAGAGCAGCGTAACGGCTTCATCCAAAGCTTGAAGGATGAGCCCTCT
N E E Q R N G F I Q S L K D E P S
HindIII

310 320 330 340 350
CAGTCTGCGAATCTGCTAGCGGATGCCAAGAAACTGAACGATGCGCAGGC
Q S A N L L A D A K K L N D A Q A
NheI FspI

360 370 380 390 400 ACCGAAATCGGGTCAGGGGCAATTCATGGCTGACAACAAATTCAACAAGG P K S D Q G Q F M A D N K F N K

410 420 430 440 450
AACAGCAGAACGCGTTCTACGAGATCTTGCACCTGCCGAACCTGAACGAA
E Q Q N A F Y E I L H L P N L N E
MluI BglII BspMI+

460 470 480 490 500 GAGCAGCGTAACGCTTCATCCAAAGCTTGAAGGATGAGCCCTCTCAGTC E Q R N G F I Q S L K D E P S Q S HindIII

FIG. 21B-1

510 520 530 540 550
TGCGAATCTGCTAGCGGATGCCAAGAAACTGAACGATGCGCAGGCACCGA
A N L L A D A K K L N D A Q A P
NheI FspI

560 570 580 590 600
AGGATCCTAATGGGCTGTACGTCGACTTCAGCGACGTGGGCTGGGACGAC
K D P N G L Y V D F S D V G W D D
Bamhi Sali

610 620 630 640 650
TGGATTGTGGCCCCACCAGGCTACCAGGCCTTCTACTGCCATGGCGAATG
W I V A P P G Y Q A F Y C H G E C
Stul Ncol Bsml+

660 670 680 690 700
CCCTTTCCCGCTAGCGATCACTTCAACAGCACCAACCACGCCGTGGTGC
PFPLADHFNSTNHAVV
NheI DraIII
PflMI

į,

710 720 730 740 750 AGACCCTGGTGAACTCTGTCAACTCCAAGATCCCTAAGGCTTGCTGCGTG Q T L V N S V N S K I P K A C C V MstII

760 770 780 790 800 CCCACCGAGCTGTCCGCCATCAGCATGCTGTACCTGGACGAGAATGAGAA PTELSAISMLYLDENEK SphI

810 820 830 840 850 GGTGGTGCTGAAGAACTACCAGGAGATGGTAGTAGAGGGCTGCGCTGCC V V L K N Y Q E M V V E G C G C Pf1MI

860 GCTAACTGCAG R * PstI

FIG. 21B-2

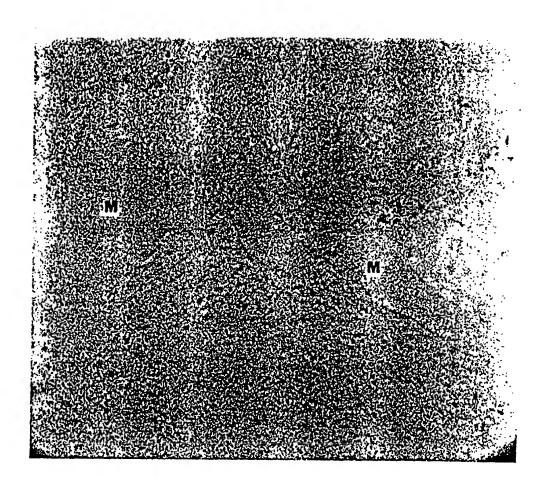


FIG. 22A

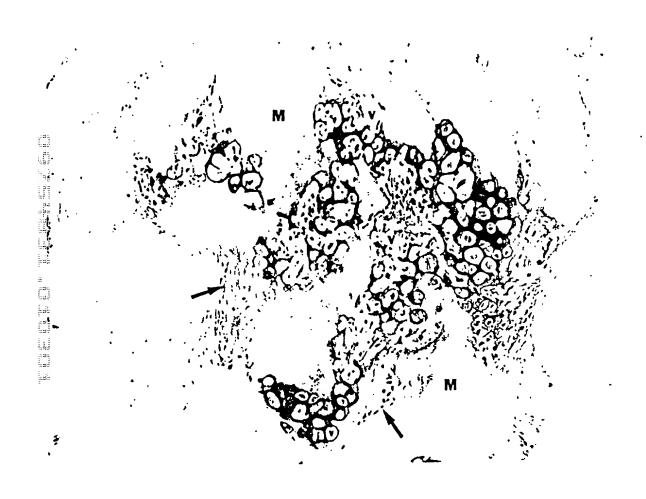


FIG. 22B